

REMARKS

Priority

U.S. Serial No. 09/170,980 is a divisional application of the parent application, U.S. Serial No. 08/790,137. Parent application update status for U.S. Application No. 08/790,137, filed January 29, 1997, now U.S. Patent No. 5,840,871 was requested by the Examiner.

Sequence Listing

In accordance with the requirements of 37 CFR §1.821- 1.825, Applicants hereby submit one (1) diskette containing the computer-readable information for the "Sequence Listing". The diskette complies with the requirements of 37 CFR §1.824 and is IBM PC compatible using a UNIX operating system with PERL Program.

Accompanying the response is the paper copy of the Sequence Listing as disclosed in the application.

The content of the "Sequence Listing" paper copy is identical to the computer readable copy, as required under 37 CFR § 1.821(f).

Applicants submit herewith a new Sequence Listing and CRF. In reviewing rejections, Applicants were puzzled by the citation of several old references having 100% identity. Applicants then discovered that SEQ ID NO:1 was inadvertently included as a duplicate of SEQ ID NO:3 rather than the amino acid sequence given in Figures 1A and 1B. Applicants regret and apologize for the inconvenience caused to the Examiner by this error.

The amended Sequence Listing and CRF contain the corrected sequence for SEQ ID NO:1 as is represented in Figures 1A, 1B and Figure 2. Support for the amended SEQ ID NO:1 as represented in Figures 1A, 1B and Figure 2, and as being 253 amino acids in length is found in the specification on page 3, lines 1-2, and lines 5-7, and page 11, lines 5-8, respectively and in Figures 1A, 1B, and Figure 2. No new matter is added by any of these amendments.

The rejections are thus moot, as the examination was directed to an incorrect representation of the sequence indicated as SEQ ID NO:1. The rejections under 35 U.S.C. § 101 and 35 U.S.C. § 112 first and second paragraphs, and § 102 in particular are moot as the polypeptide sequence this rejection was based upon has been amended. Applicants respectfully request re-examination of claims as directed to amended SEQ ID NO:1, and again apologize for

their error.

In spite of this amendment, Applicants can respond to the Examiner's rejection based on lack of a written description. Written description of common structural and functional attributes shared by members of the genus is described in the specification on page 11, lines 10-17. Furthermore, the description in functional language of the polypeptide sequence as having chymotrypsinogen-like activity defines a common attribute that identifies a member of a genus. See also page 11, lines 12-13. Additional attributes of the genus are described on page 1, lines 15-23.

The rejection of claims 1, 19 and 20 under 35 U.S.C. § 112, first paragraph, for lack of enablement for any polypeptides comprising functional fragments or homology to SEQ ID NO:1, now amended, is objected to on the following grounds. Fragment synthesis is described on page 23, lines 7-13. The resulting proteins, homologs to SEQ ID NO:1, now amended, or fragments thereof, can be utilized in the practice of the invention as described on page 19, line 27 through page 20, line 15. Descriptions which enable one of ordinary skill in the art to express the resulting peptide sequence(s), and assays for activity are described on page 44, lines 6-27. Reference is provided to one skilled in the art to practice the invention as used in pharmaceutical compositions on page 28, line 27 through page 31, line 10.

Rejections of claims 1 and 20 based on 35 U.S.C. § 102(b) as being anticipated by Lin et al. and Shine et al., are rendered moot in view of the amended SEQ ID NO:1, which has only 44.1% identity to Lin et al. and 44.5% identity to Shine et al. as illustrated by use of the Lasargene MegAlign sequence alignment tool (see attached Exhibit A). This low level of percent identity indicates that amended SEQ ID NO:1 was not patented more than one year prior to the date of application for patent in the United States.

Rejections of claims 1 and 18-20 based on 35 U.S.C. § 102(e) as being anticipated by Au-Young et al. or Bandman et al., are rendered moot in view of the amended SEQ ID NO: 1, which has only 49.8% and 49.4% identity respectively. Thus, as illustrated by use of the Lasargene MegAlign sequence alignment tool (see attached Exhibit B), amended SEQ ID NO:1 has not been described in a patent granted to another.

Rejections of claims 1 and 18 under 35 U.S.C. § 102(b) as being anticipated by Evans et al., Baker et al., Angermann et al., and Lu et al., are rendered moot in view the amended SEQ ID

NO:1, which has only 49.4% identity to each of these sequences. Evans was selected as the sequence example, as illustrated by use of the Lasergene MegAlign sequence alignment tool (see attached Exhibit B). Therefore amended SEQ ID NO:1 was not described in a printed publication. Results of the Lasergene analyses are included to assist the Examiner.

CONCLUSION

In light of the above amendments and remarks, Applicants respectfully request that the Examiner re-examine the claims to ensure that they are free of the prior art, and submit that the present application is in condition for allowance.

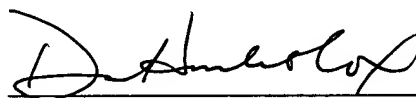
If the Examiner contemplates other action, or if a telephone conference would expedite allowance of the claims, Applicants invite the Examiner to contact Applicants' Attorney at (650)855-0555.

Applicants believe that no fee is due with this communication. However, if the USPTO determines that a fee is due, the Commissioner is hereby authorized to charge Deposit Account No. 09-0108. This form is enclosed in duplicate.

Respectfully submitted,

INCYTE GENOMICS, INC.

Date: 30 June 2000

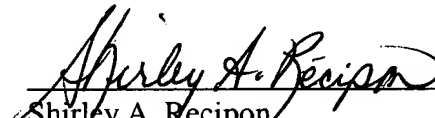


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-----A P P I Q S R I V G G W E C E Q H S Q P W Q A										Majority	
	10		20		30		40				
1	M W F L V L C L A L S L G G T G A A P P I Q S R I V G G W E C E Q H S Q P W Q A										SEQIDNO1
1	-----A P P I Q S R I V G G W E C E Q H S Q P W Q A										lin
1	-----A P P I Q S R I V G G W E C E Q H S Q P W Q A										shine
A L Y H F S T F Q C G G I L V H R Q W V L T A A H C I S D N Y Q L W L G R H N L										Majority	
	50		60		70		80				
41	A L Y Q K T R L L C G A T X X A P R W F L T A A H C L K P R Y I V H L G Q H N L										SEQIDNO1
24	A L Y H F S T F Q C G G I L V H R Q W V L T A A H C I S D N Y Q L W L G R H N L										lin
24	A L Y H F S T F Q C G G I L V H R Q W V L T A A H C I S D N Y Q L W L G R H N L										shine
F D D E N T A Q F V H V S E S F P H P G F N M S L L E N H T R Q A D E D Y S H D										Majority	
	90		100		110		120				
81	Q K E E G C E Q T R T A T E S F P H P G F N N S L - - - - - P N K D H R N D										SEQIDNO1
64	F D D E N T A Q F V H V S E S F P H P G F N M S L L E N H T R Q A D E D Y S H D										lin
64	F D D E N T A Q F V H V S E S F P H P G F N M S L L E N H T R Q A D E D Y S H D										shine
L M L L R L T E P A D T I T D A V K V V E L P T Q E P E V G S T C L A S G W G S										Majority	
	130		140		150		160				
114	I M L V K M A S P V - S I T W A V R P L T L S S R C V T A G T S C L I S G W G S										SEQIDNO1
104	L M L L R L T E P A D T I T D A V K V V E L P T Q E P E V G S T C L A S G W G S										lin
104	L M L L R L T E P A D T I T D A V K V V E L P T Q E P E V G S T C L A S G W G S										shine
I E P E N F S F P D D L Q C V D L K I L P N D E C E K A H V Q K V T D F M L C V										Majority	
	170		180		190		200				
153	T S S P Q L R L P H T L R C A N I T I I E H Q K C E N A Y P G N I T D T M V C A										SEQIDNO1
144	I E P E N F S F P D D L Q C V D L K I L P N D E C K K A H V Q K V T D F M L C V										lin
144	I E P E N F S F P D D L Q C V D L K I L P N D E C E K A H V Q K V T D F M L C V										shine
G H L E G G K D T C V G D S G G P L M C D G V L Q G V T S W G Y V P C G T P N K										Majority	
	210		220		230		240				
193	S V Q E G G K D S C Q G D S G G P L V C N Q S L Q G I I S W G Q D P C A I T R K										SEQIDNO1
184	G H L E G G K D T C V G D S G G P L M C D G V L Q G V T S W G Y V P C G T P N K										lin
184	G H L E G G K D T C V G D S G G P L M C D G V L Q G V T S W G Y V P C G T P N K										shine
P S V A V R V L S Y V K W I E D T I A E N S										Majority	
	250		260								
233	P G V Y T K V C K Y V D W I Q E T M - K N N										SEQIDNO1
224	P S V A V R V L S Y V K W I E D T I A E N S										lin
224	P S V A V R V L S Y V K W I E D T I A E N S										shine

Decoration 'Decoration #1': Shade (with solid black) residues that match SEQIDNO1 exactly.

Percent Similarity									
Percent Divergence		1	2	3					
	1		44.1	44.5	1	SEQIDNO1			
	2	83.3		99.6	2	lin			
	3	82.2	0.4		3	shine			
		1	2	3					

1	MWFLVLCCLALS	SLGGTGAAPP	IQSRIVGGWEC	EQHSQPWQA	SEQIDNO1																		
1	MWFLVLCCLALS	SLGGTGAAPP	IQSRIVGGWEC	EQHSQPWQA	evans																		
1	MWFLVLCCLALS	SLGGTGAAPP	IQSRIVGGWEC	EQHSQPWQA	Bandman																		
1	MWFLVLCCLALS	SLGGTGAAPP	IQSRIVGGWEC	EQHSQPWQA	au-young																		
41	ALYQKTRLLCGAT	XXAPRWFLTA	AHCLKPRYIV	HLGQHNL	SEQIDNO1																		
41	ALYHFSTFQCG	GILVHRQWV	LTAAHCI	SDNYQLWLGR	HNL	evans																	
41	ALYHFSTFQCG	GILVHRQWV	LTAAHCI	SDNYQLWLGR	HNL	Bandman																	
41	ALYHFSTFQCG	GILVHRQWV	LTAAHCI	SDNYQLWLGR	HNL	au-young																	
81	QKEEGCEQTRT	ATESFPHPGFN	NSL	- - - - -	PNKDHRND	SEQIDNO1																	
81	FDDENTAQQFV	HVSESFPHPGFN	MSL	LENHTRQADE	DYSHD	evans																	
81	FDDENTAQQFV	HVSESFPHPGFN	MSL	LENHTRQADE	DYSHD	Bandman																	
81	FDDENTAQQFV	HVSESFPHPGFN	MSL	LENHTRQADE	DYSHD	au-young																	
114	IMLVKMASPV	-SITWAVRPL	TLSSRCVTAG	GTSC	LISGWGS	SEQIDNO1																	
121	LMLLRLTEPA	DTITDAVKV	VELPTQEPEV	GST	CLASGWGS	evans																	
121	LMLLRLTEPA	DTITDAVKV	VELPTQEPEV	GST	CLASGWGS	Bandman																	
121	LMLLRLTEPA	DTITDAVKV	VELPTQEPEV	GST	CLASGWGS	au-young																	
153	TSSPQLRLPHT	LRCANITII	IEHQKCE	NAYPGNIT	DTMVCA	SEQIDNO1																	
161	IEPENFSFP	DDLQCVDLK	ILPNDECK	KAHVQKV	TDFMLC	V evans																	
161	IEPENFSFP	DDLQCVDLK	ILPNDECK	KAHVQKV	TDFMLC	V Bandman																	
161	IEPENFSFP	DDLQCVDLK	ILPNDECK	KAHVQKV	TDFMLC	V au-young																	
193	SVQEGGKDS	CQGD	SGGPLV	CNQSLQGI	ISWGQD	PCAITRK	SEQIDNO1																
201	GHL	EGGKD	TCVGD	SGGPL	MC	DGVLQGV	TSWGYV	PCGTPNK	evans														
201	GHL	EGGKD	TCVGD	SGGPL	MC	DGVLQGV	TSWGYV	PCGTPNK	Bandman														
201	GHL	EGGKD	TCVGD	SGGPL	MC	DGVLQGV	TSWGYV	PCGTPNK	au-young														
233	P	G	V	Y	T	K	V	C	K	Y	V	D	W	I	Q	E	T	M	-	K	N	N	SEQIDNO1
241	P	S	V	A	V	R	V	L	S	Y	V	K	W	I	E	D	T	I	A	E	N	S	evans
241	P	S	V	A	V	R	V	L	S	Y	V	K	W	I	E	D	T	I	A	E	N	S	Bandman
241	P	S	V	A	V	R	V	L	S	Y	V	K	W	I	E	D	T	I	A	E	N	S	au-young

Decoration 'Decoration #1': Shade (with solid black) residues that match SEQIDNO1 exactly.

Percent Similarity							
Percent Divergence		1	2	3	4		
	1		49.4	49.4	49.8	1	SEQIDNO1
	2	74.2		100.0	99.6	2	evans
	3	74.2	0.0		99.6	3	Bandman
	4	73.2	0.4	0.4		4	au-young
	1	2	3	4			